C L A I M S

1. Probe consisting of at least about 15 nucleotides of the transcribed spacer region between the 16S and 23S rRNA genes of prokaryotic organisms, and more particularly bacteria, and preferably from about 15 nucleotides to about the maximum number of nucleotides of the spacer refion and more preferably from about 15 to about 100 nucleotides.

2. Probe according to claim 1, for use in a hybridization assay, liable to be obtained in the process which comprises constructing an oligonucleotide that is sufficiently complementary to hybridize to a sequence of the spacer region between rRNA genes, particularly the spacer region between the 16S rRNA gene and the 23S rRNA gene, selected to be unique to non-viral organisms, particularly prokaryotic organisms, more particularly bacteria, sought to be detected, with said sequence of the spacer region between rRNA genes being selected

- either by
  - * comparing the nucleotide sequence of the spacer region between the rRNA genes of the sought organism with the nucleotide sequence of the spacer region between the rRNA genes of the closest neighbours,
  - * selecting a sequence of at least 15 nucleotides, and preferably from about 15 to about the maximum number of nucleotides of the spacer region, and more preferably from about 15 to about 100 nucleotides of the spacer region between rRNA genes of the sought organism which presents at least one mismatch with the spacer region between the rRNA genes of at least one of the closest neighbours,

- or by
  - * deleting, in the spacer region between th rRNA genes of the organism to be sought, the tRNA genes and possibly the signal sequences, to obtain a shortened spacer region and
  - * determining by trial and error a specific nucleotide sequence of at least about 15 nucleotides, and preferably from about 15 to about the maximum number of nucleotides of the spacer region, and more preferably from about 15 to about 100 nucleotides, from the shortened spacer region, said sequence being able to hybridize specifically with the nucleic acids (DNA and/or RNAs) of the sought organism.

3. Probe according to anyone of claims 1 or 2, containing

- either a sequence belonging to a nucleic acid selected from the following group of nucleic acids and which includes from 15 to the maximum number of nucleotides of the selected nucleic acid:

Group NGI1:	
CGATGCGTCG TTATTCTACT TCGC	NGI1
GCGAAGTAGA ATAACGACGC ATCG	NGI1IC
GCGAAGUAGA AUAACGACGC AUCG	NGI1ICR
CGAUGCGUCG UUAUUCUACU UCGC	NGI1R
Group NGI2:	
TTCGTTTACC TACCCGTTGA CTAAGTAAGC AAAC	NGI2
GTTTGCTTAC TTAGTCAACG GGTAGGTAAA CGAA	NGI2IC
GUUUGCUUAC UUAGUCAACG GGUAGGUAAA CGAA	NGI2ICR
UUGGUUUACC UACCCGUUGA CUAAGUAAGC AAAC	NGI2R
Group NMI1:	
GGTCAAGTGT GACGTCGCCC TG	NMI1
CAGGGCGACG TCACACTTGA CC	NMI1IC

CAGGGCGACG UCACACUUGA CC NMI1ICR
GGUCAAGUGU GACGUCGCCC UG NMI1R

Group NMI2:
GTTCTTGGTC AAGTGTGACG TC NMI2
GACGTCACAC TTGACCAAGA AC NMI2IC
GACGUCACAC UUGACCAAGA AC NMI2ICR
GUUCUUGGUC AAGUGUGACG UC NMI2R

Group NMI3:
GCGTTCGTTA TAGCTATCTA CTGTGC NMI3
GCACAGTAGA TAGCTATAAC GAACGC NMI3IC
GCACAGUAGA UAGCUAUAAC GAACGC NMI3ICR
GCGUUCGUUA UAGCUAUCUA CUGUGC NMI3R

Group NMI4:
TGCGTTCGAT ATTGCTATCT ACTGTGCA NMI4
TGCACAGTAG ATAGCAATAT CGAACGCA NMI4IC
UGCACAGUAG AUAGCAAUAU CGAACGCA NMI4ICR
UGCGUUCGAU AUUGCUAUCU ACUGUGCA NMI4R

Group NMI5:
TTTTGTTCTTGGTCAAGTGTGACGTCGCCCTGAATGGATTCTGTTCCATT
NMI5
AATGGAACAGAATCCATTCAGGGCGACGTCACACTTGACCAAGAACAAAA
NMI5C
AAUGGAACAGAAUCCAUUCAGGGCGACGUCACACUUGACCAAGAACAAAA
NMI5ICR
UUUUGUUCUUGGUCAAGUGUGACGUCGCCCUGAAUGGAUUCUGUUCCAUU
NMI5R

Group NMI6
TTTGCCTAAC ATTCCGTTGA CTAGAACATC AGAC NMI6
GTCTGATGTT CTAGTCAACG GAATGTTAGG CAAA NMI6IC
GUCUGAUGUU CUAGUCAACG GAAUGUUAGG CAAA NMI6ICR
UUUGCCUAAC AUUCCGUUGA CUAGAACAUC AGAC NMI6R

Group HDI1:

TTATTATGCG CGAGGCATAT TG	HDI1
CAATATGCCT CGCGCATAAT AA	HDI1IC
CAAUAUGCCU CGCGCAUAAU AA	HDI1ICR
UUAUUAUGCG CGAGGCAUAU UG	HDI1R
Group BCI1:	
TTAAACATCT TACCAAAG	BCI1
CTTTGGTAAG ATGTTTAA	BCI1IC
CUUUGGUAAG AUGUUUAA	BCI1ICR
UUAAACAUCU UACCAAAG	BCI1R
Group BCI2:	
TTGATGTTTA AACTTGCTTG GTGGA	BCI2
TCCACCAAGC AAGTTTAAAC ATCAA	BCI2IC
UCCACCAAGC AAGUUUAAAC AUCAA	BCI2ICR
UUGAUGUUUA AACUUGCUUG GUGGA	BCI2R
Group BPI1:	
CCACACCCAT CCTCTGGACA GGCTT	BPI1
AAGCCTGTCC AGAGGATGGG TGTGG	BPI1IC
AAGCCUGUCC AGAGGAUGGG UGUGG	BPI1ICR
CCACACCCAU CCUCUGGACA GGCUU	BPI1R
Group HII1:	
ACGCATCAAA TTGACCGCAC TT	HII1
AAGTGCGGTC AATTTGATGC GT	HII1IC
AAGUGCGGUC AAUUUGAUGC GU	HII1ICR
ACGCAUCAAA UUGACCGCAC UU	HII1R
Group HII2:	
ACTTTGAAGT GAAAACTTAA AG	HII2
CTTTAAGTTT TCACTTCAAA GT	HII2IC
CUUUAAGUUU UCACUUCAAA GU	HII2ICR
ACUUUGAAGU GAAAACUUAA AG	HII2R
Group SAI1:	
AATCGAAAGG TTCAAATTGT T	SAI1
AACAATTTGA ACCTTTCGAT T	SAI1IC

AACAAUUUGA ACCUUUCGAU U	SAI1ICR
AAUCGAAAGG UUCAAAUUGU U	SAI1R
Group SAI2:	
GGAAACCTGC CATTTGCGTC TT	SAI2
AAGACGCAAA TGGCAGGTTT CC	SAI2IC
AAGACGCAAA UGGCAGGUUU CC	SAI2ICR
GGAAACCUGC CAUUUGCGUC UU	SAI2R
Group SAI3:	
TCCACGATCT AGAAATAGAT TGTAGAA	SAI3
TTCTACAATC TATTTCTAGA TCGTGGA	SAI3IC
UUCUACAAUC UAUUUCUAGA UCGUGGA	SAI3ICR
UCCACGAUCU AGAAAUAGAU UGUAGAA	SAI3R
Group SAI4:	
TCTAGTTTTA AAGAAACTAG GTT	SAI4
AACCTAGTTT CTTTAAAACT AGA	SAI4IC
AACCUAGUUU CUUUAAAACU AGA	SAI4ICR
UCUAGUUUUA AAGAAACUAG GUU	SAI4R
Group SPI1:	
GTGAGAGATC ACCAAGTAAT GCA	SPI1
TGCATTACTT GGTGATCTCT CAC	SPI1IC
UGCAUUACUU GGUGAUCUCU CAC	SPI1ICR
GUGAGAGAUC ACCAAGUAAU GCA	SPI1R
Group SPI2	
AGGAACTGCG CATTGGTCTT	SPI2
AAGACCAATG CGCAGTTCCT	SPI2IC
AAGACCAAUG CGCAGUUCCU	SPI2ICR
AGGAACUGCG CAUUGGUCUU	SPI2R
Group SPI3	
GAGTTTATGA CTGAAAGGTC AGAA	SPI3
TTCTGACCTT TCAGTCATAA ACTC	SPI3IC
UUCUGACCUU UCAGUCAUAA ACUC	SPI3ICR
GAGUUUAUGA CUGAAAGGUC AGAA	SPI3R

- or a variant sequence which distinguishes of any of the preceding sequences:
  * either by addition to or removal from any of their respective extremities of one or several nucleotides;
  * or changing within any of said sequences of one or more nucleotides;
  * or both;

yet provided that in any of the above circumstances said probe still hybridizes with the same RNA or DNA target as the corresponding unmodified sequence.

4. Probe for detecting one or more Neisseria gonorrhoeae strains, containing:

- either a sequence belonging to a nucleic acid selected from the following groups of nucleic acids and which includes from 15 to the maximum number of nucleotides of the selected nucleic acid:

Group NGI1:

CGATGCGTCG TTATTCTACT TCGC	NGI1
GCGAAGTAGA ATAACGACGC ATCG	NGI1IC
GCGAAGUAGA AUAACGACGC AUCG	NGI1ICR
CGAUGCGUCG UUAUUCUACU UCGC	NGI1R

Group NGI2:

TTCGTTTACC TACCCGTTGA CTAAGTAAGC AAAC	NGI2
GTTTGCTTAC TTAGTCAACG GGTAGGTAAA CGAA	NGI2IC
GUUUGCUUAC UUAGUCAACG GGUAGGUAAA CGAA	NGI2ICR
UUGGUUUACC UACCCGUUGA CUAAGUAAGC AAAC	NGI2R

- or a variant sequence which distinguishes of any of the preceding sequences:
  * either by addition to or removal from any of their respective extremities of one or several nucleotides;

* or changing within any of said sequences of one or more nucleotides;
* or both;

yet provided that in any of the above circumstances said probe still hybridizes with the same RNA or DNA target as the corresponding unmodified sequence.

5. Process for detecting Neisseria gonorrhoeae strains in a biological sample, wherein said process comprises contacting said biological sample - in which the nucleic acids (DNAs and/or RNAs) of the strains have been made accessible to hybridization, if need be, under suitable denaturation conditions, with said nucleic acid to be detected being possibly amplified using the polymerase chain reaction, with two primers, more preferably two more evolutionarily conserved primers, flanking the target sequence of the probe - with a probe according to any of the probes of claim 4 under conditions enabling hybridization between the probe and complementary nucleic acids of the Neisseria gonorrhoeae strains, which may be present in the sample, and detecting the hybrids possibly formed, particularly with a probe hybridizing to both DNA and RNA of a Neisseria gonorrhoeae strain which may be present in the biological sample.

6. Process for detecting Neisseria gonorrhoeae, in a biological sample, according to claim 5, wherein:
the hybridization medium contains about 3 x SSC, (SSC = 0.15 M NaCl, 0.015 M sodium citrate, pH 7.0) about 25 mM of phosphate buffer pH 7.1, 20% deionized formamide, 0.02% Ficoll, 0.02% bovine serum albumin, 0.02% polyvinylpyrrolidone, and about 0.1 mg/ml sheared, denatured salmon sperm DNA,
and/or
the wash medium contains about 3 x SSC, 25 mM phosphate buffer pH 7.1, and 20% deionized formamide and wherein the probe used is any of the probes of claim 4, the

hybridization temperatur being suitably adjusted to the range of ab ut 50°C and/or the wash temperature to the rang of about 50°C, and particularly wherein said target sequence and the corresponding relevant hybridization temperature (HT) and wash temperature (WT), respectively, are as follows:

GCGAAGTAGA ATAACGACGC ATCG

HT and/or WT: 50 °C.

GUUUGCUUAC UUAGUCAACG GGUAGGUAAA CGAA

HT and/or WT: 50 °C.

7. Kit for the detection in vitro of a large number, preferably all Neisseria gonorrhoeae strains in a biological sample, with said kit containing:

either

- at least one probe selected among any of those according to claim 4;
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a large number, preferably all strains of Neisseria gonorrhoeae to be carried out;
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least two probes, targeting the same nucleic acid molecule, and of which at least one is specific for Neisseria gonorrhoeae and which is selected from any one of the probes of claim 4,
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Neisseria gonorrhoeae to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least one probe select d among any of those according to claim 4, which is fixed to a solid support,
- the primers needed for performing enzymatic amplification of the DNA and/or RNA containing the target sequence of the above-mentioned probe, when appropriate,
- the buffers or components necessary for producing the buffers enabling enzymatical amplification and/or enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Neisseria gonorrhoeae to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate.

8. Probe for detecting one or more Neisseria meningitidis strains, containing:

- either a sequence belonging to a nucleic acid selected from the following group of nucleic acids and which includes from 15 to the maximum number of nucleotides of the selected nucleic acid:

Group NMI1:

GGTCAAGTGT GACGTCGCCC TG	NMI1
CAGGGCGACG TCACACTTGA CC	NMI1IC
CAGGGCGACG UCACACUUGA CC	NMI1ICR
GGUCAAGUGU GACGUCGCCC UG	NMI1R

Group NMI2:

GTTCTTGGTC AAGTGTGACG TC	NMI2
GACGTCACAC TTGACCAAGA AC	NMI2IC
GACGUCACAC UUGACCAAGA AC	NMI2ICR
GUUCUUGGUC AAGUGUGACG UC	NMI2R

Group NMI3:

GCGTTCGTTA TAGCTATCTA CTGTGC	NMI3
GCACAGTAGA TAGCTATAAC GAACGC	NMI3IC
GCACAGUAGA UAGCUAUAAC GAACGC	NMI3ICR

GCGUUCGUUA UAGCUAUCUA CUGUGC NMI3R

Group NMI4:

TGCGTTCGAT ATTGCTATCT ACTGTGCA NMI4

TGCACAGTAG ATAGCAATAT CGAACGCA NMI4IC

UGCACAGUAG AUAGCAAUAU CGAACGCA NMI4ICR

UGCGUUCGAU AUUGCUAUCU ACUGUGCA NMI4R

Group NMI5:

TTTTGTTCTTGGTCAAGTGTGACGTCGCCCTGAATGGATTCTGTTCCATT NMI5

AATGGAACAGAATCCATTCAGGGCGACGTCACACTTGACCAAGAACAAAA NMI5C

AAUGGAACAGAAUCCAUUCAGGGCGACGUCACACUUGACCAAGAACAAAA NMI5ICR

UUUUGUUCUUGGUCAAGUGUGACGUCGCCCUGAAUGGAUUCUGUUCCAUU NMI5R

Group NMI6:

TTTGCCTAAC ATTCCGTTGA CTAGAACATC AGAC NMI6

GTCTGATGTT CTAGTCAACG GAATGTTAGG CAAA NMI6IC

GUCUGAUGUU CUAGUCAACG GAAUGUUAGG CAAA NMI6ICR

UUUGCCUAAC AUUCCGUUGA CUAGAACAUC AGAC NMI6R

- or a variant sequence which distinguishes of any of the preceding sequences:
  - * either by addition to or removal from any of their respective extremities of one or several nucleotides;
  - * or changing within any of said sequences of one or more nucleotides;
  - * or both;

yet provided that in any of the above circumstances said probe still hybridizes with the same RNA or DNA target as the corresponding unmodified sequence.

9. Process for detecting Neisseria meningitidis strains in a biological sample, wherein said process

comprises contacting said biological sample - in which the nucleic acids (DNAs and/or RNAs) of the strains have been made accessible to hybridization, if need be, under suitable denaturation conditions, with said nucleic acid to be detected being possibly amplified using the polymerase chain reaction, with two primers, more preferably two more evolutionarily conserved primers, flanking the target sequence of the probe - with a probe according to any one of claim 8 under conditions enabling hybridization between the probe and complementary nucleic acids of the Neisseria meningitidis strains, which may be present in the sample, and detecting the hybrids possibly formed particularly with a probe hybridizing to both DNA and RNA of a Neisseria meningitidis strain which may be present in the biological sample.

10. Process for detecting Neisseria meningitidis, in a biological sample, according to claim 9, wherein:
the hybridization medium contains about 3 x SSC, (SSC = 0.15 M NaCl, 0.015 M sodium citrate, pH 7.0) about 25 mM of phosphate buffer pH 7.1, 20% deionized formamide, 0.02% Ficoll, 0.02% bovine serum albumin, 0.02% polyvinylpyrrolidone, and about 0.1 mg/ml sheared, denatured salmon sperm DNA,
and/or
the wash medium contains about 3 x SSC, 25 mM phosphate buffer pH 7.1, and 20% deionized formamide and wherein the probe used is anyone of the probes of claim 8, the hybridization temperature being suitably adjusted to the range of about 40 to 58°C and/or the wash temperature to the range of about 40 to 58°C, and particularly, wherein said target sequence and the corresponding relevant hybridization temperature (HT) and wash temperature (WT), respectively, are as follows:
CAGGGCGACG TCACACTTGA CC

HT and/or WT: 45°C
GACGTCACAC TTGACCAAGA AC
HT and/or WT: 45°C
GCACAGTAGA TAGCTATAAC GAACGC
HT and/or WT: 40°C
TGCACAGTAG ATAGCAATAT CGAACGCA
HT and/or WT: 48°C
TTTTGTTCTTGGTCAAGGTGTGACGTCGCCCTGAATGGATTCTGTTCCATT
HT and/or WT: 58°C
GTCTGATGTT CTAGTCAACG GAATGTTAGG CAAA
HT and/or WT: 50°C

11. Kit for the detection in vitro of a large number, preferably all Neisseria meningitidis strains in a biological sample, with said kit containing:

either

- at least one probe selected among any of those according to claim 8;
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a large number, preferably all strains of Neisseria meningitidis to be carried out;
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least two probes, targeting the same nucleic acid molecule, and of which at least one is specific for Neisseria meningitidis and which is selected from any one of the probes of claim 8,
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Neisseria meningitidis to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least one probe selected among any of those according to claim 4, which is fixed to a solid support,
- the primers needed for performing enzymatical amplification of the DNA and/or RNA containing the target sequence of the above-mentioned probe, when appropriate,
- the buffer or components necessary for producing the buffers enabling enzymatical amplification and/or enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Neisseria meningitidis to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate.

12. Probe for detecting one or more Haemophilus ducreyi strains, containing:

- either a sequence belonging to a nucleic acid selected from the following group of nucleic acids and which includes from 15 to the maximum number of nucleotides of the selected nucleic acid:

Group HDI1:

TTATTATGCG CGAGGCATAT TG	HDI1
CAATATGCCT CGCGCATAAT AA	HDI1IC
CAAUAUGCCU CGCGCAUAAU AA	HDI1ICR
UUAUUAUGCG CGAGGCAUAU UG	HDI1R

- or a variant sequence which distinguishes of any of the preceding sequences:
  * either by addition to or removal from any of their respective extremities of one or several nucleotides;
  * or changing within any of said sequences of one or more nucleotides;
  * or both;

yet provided that in any of the above circumstances said probe still hybridizes with the same RNA or DNA target as the corresponding unmodified sequence.

13. Process for detecting Haemophilus ducreyi strains in a biological sample, wherein said process comprises contacting said biological sample - in which the nucleic acids (DNAs and/or RNAs) of the strains have been made accessible to hybridization, if need be, under suitable denaturation conditions, with said nucleic acid to be detected being possibly amplified using the polymerase chain reaction, with two primers, more preferably two more evolutionarily conserved primers, flanking the target sequence of the probe - with a probe according to any one of claim 12 under conditions enabling hybridization between the probe and complementary nucleic acids of the Haemophilus ducreyi strains, which may be present in the sample, and detecting the hybrids possibly formed, particularly with a probe hybridizing to both DNA and RNA of a Haemophilus ducreyi strain which may be present in the biological sample.

14. Process for detecting Haemophilus ducreyi, in a biological sample, according to anyone of claim 13, wherein:

the hybridization medium contains about 3 x SSC, (SSC = 0.15 M NaCl, 0.015 M sodium citrate, pH 7.0) about 25 mM of phosphate buffer pH 7.1, 20% deionized formamide, 0.02% Ficoll, 0.02% bovine serum albumin, 0.02% polyvinylpyrrolidone, and about 0.1 mg/ml sheared, denatured salmon sperm DNA,

and/or

the wash medium contains about 3 x SSC, 25 mM phosphate buffer pH 7.1, and 20% deionized formamide and wherein the probe used is anyone of the probes of claim 12, the hybridization temperature being suitable adjusted to th range of about 40°C and/or the wash temperatur

to the range of about 40°C, and particularly, wherein said target sequence and the corresponding relevant hybridization temperature (HT) and wash temperature (WT), respectively, are as follows:

CAATATGCCT CGCGCATAAT AA

HT and/or WT: 40 °C.

15. Kit for the detection in vitro of a large number, preferably all Haemophilus ducreyi strains in a biological sample, with said kit containing:

either

- at least one probe selected among any of those according to claim 12;
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a large number, preferably all strains of Haemophilus ducreyi to be carried out;
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least two probes, targeting the same nucleic acid molecule, and of which at least one is specific for Haemophilus ducreyi and which is selected from any one of the probes of claim 12,
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Haemophilus ducreyi to be carried out,
- means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least one probe selected among any of those according to claim 12, which is fixed to a solid support,
- the primers needed for performing enzymatical amplification of the DNA and/or RNA containing the

target sequence of the above-mentioned probe, when appropriate,

- the buffer or components necessary for producing the buffers enabling enzymatical amplification and/or enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Haemophilus ducreyi to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate.

16. Probe for detecting one or more Branhamella catarrhalis strains, containing:

- either a sequence belonging to a nucleic acid selected from the following group of nucleic acids and which includes from 15 to the maximum number of nucleotides of the selected nucleic acid:

Group BCI1:

TTAAACATCT TACCAAAG	BCI1
CTTTGGTAAG ATGTTTAA	BCI1IC
CUUUGGUAAG AUGUUUAA	BCI1ICR
UUAAACAUCU UACCAAAG	BCI1R

Group BCI2:

TTGATGTTTA AACTTGCTTG GTGGA	BCI2
TCCACCAAGC AAGTTTAAAC ATCAA	BCI2IC
UCCACCAAGC AAGUUUAAAC AUCAA	BCI2ICR
UUGAUGUUUA AACUUGCUUG GUGGA	BCI2R

- or a variant sequence which distinguishes of any of the preceding sequences:
  * either by addition to or removal from any of their respective extremities of one or several nucleotides;
  * or changing within any of said sequences of one or more nucleotides;
  * or both;

yet provid d that in any of the above circumstances said probe still hybridizes with the same RNA or DNA target as the corresponding unmodified sequence.

17. Process for detecting Branhamella catarrhalis strains in a biological sample, wherein said process comprises contacting said biological sample - in which the nucleic acids (DNAs and/or RNAs) of the strains have been made accessible to hybridization, if need be, under suitable denaturation conditions, with said nucleic acid to be detected being possibly amplified using the polymerase chain reaction, with two primers, more preferably two more evolutionarily conserved primers, flanking the target sequence of the probe - with a probe according to any one of claim 16 under conditions enabling hybridization between the probe and complementary nucleic acids of the Branhamella catarrhalis strains, which may be present in the sample, and detecting the hybrids possibly formed, particularly with a probe hybridizing to both DNA and RNA of a Branhamella catarrhalis strain which may be present in the biological sample.

18. Process for detecting Branhamella catarrhalis, in a biological sample, according to claim 17, wherein: the hybridization medium contains about 3 x SSC, (SSC = 0.15 M NaCl, 0.015 M sodium citrate, pH 7.0) about 25 mM of phosphate buffer pH 7.1, 20% deionized formamide, 0.02% Ficoll, 0.02% bovine serum albumin, 0.02% polyvinylpyrrolidone, and about 0.1 mg/ml sheared, denatured salmon sperm DNA,
and/or
the wash medium contains about 3 x SSC, 25 mM phosphate buffer pH 7.1, and 20% deionized formamide and wherein the probe used is anyone of the probes of claim 16, the hybridization temperature being suitable adjusted to the range of about 30°C to 42°C and/or the wash temperature to the range of about 30°C to 42°C, and

particularly, wherein said target sequence and the corresponding relevant hybridization temperature (HT) and wash temperature (WT), respectively, are as follows:

CTTTGGTAAG ATGTTTAA

HT and/or WT: 30°C

TCCACCAAGC AAGTTTAAAC ATCAA

HT and/or WT: 42°C

19. Kit for the detection in vitro of a large number, preferably all Branhamella catarrhalis strains in a biological sample, with said kit containing:

either

- at least one probe selected among any of those according to claim 16;
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a large number, preferably all strains of Branhamella catarrhalis to be carried out;
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least two probes, targeting the same nucleic acid molecule, and of which at least one is specific for Branhamella catarrhalis and which is selected from any one of the probes of claim 16,
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Branhamella catarrhalis to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least one probe selected among any of those according to claim 16, which is fixed to a solid support,

- the primers needed for performing enzymatical amplification of the DNA and/or RNA containing the target sequence of the above-mentioned probe, when appropriate,
- the buffer or components necessary for producing the buffers enabling enzymatical amplification and/or enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Branhamella catarrhalis to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate.

20. Probe for detecting one or more Bordetella pertussis strains, containing:

- either a sequence belonging to a nucleic acid selected from the following group of nucleic acids and which includes from 15 to the maximum number of nucleotides of the selected nucleic acid:

Group BPI1:

CCACACCCAT CCTCTGGACA GGCTT	BPI1
AAGCCTGTCC AGAGGATGGG TGTGG	BPI1IC
AAGCCUGUCC AGAGGAUGGG UGUGG	BPI1ICR
CCACACCCAU CCUCUGGACA GGCUU	BPI1R

- or a variant sequence which distinguishes of any of the preceding sequences:
  * either by addition to or removal from any of their respective extremities of one or several nucleotides;
  * or changing within any of said sequences of one or more nucleotides;
  * or both;

yet provided that in any of the above circumstances said probe still hybridizes with the same RNA or DNA target as the corresponding unmodified sequence.

21. Process for detecting Bordetella pertussis strains in a biological sample, wherein said process comprises contacting said biological sample - in which the nucleic acids (DNAs and/or RNAs) of the strains have been made accessible to hybridization, if need be, under suitable denaturation conditions, with said nucleic acid to be detected being possibly amplified using the polymerase chain reaction, with two primers, more preferably two more evolutionarily conserved primers, flanking the target sequence of the probe - with a probe according to any one of claim 20 under conditions enabling hybridization between the probe and complementary nucleic acids of the Bordetella pertussis strains, which may be present in the sample, and detecting the hybrids possibly formed, particularly with a probe hybridizing to both DNA and RNA of a Bordetella pertussis strain which may be present in the biological sample.

22. Process for detecting Bordetella pertussis, in a biological sample, according to claim 21, wherein:
the hybridization medium contains about 3 x SSC, (SSC = 0.15 M NaCl, 0.015 M sodium citrate, pH 7.0) about 25 mM of phosphate buffer pH 7.1, 20% deionized formamide, 0.02% Ficoll, 0.02% bovine serum albumin, 0.02% polyvinylpyrrolidone, and about 0.1 mg/ml sheared, denatured salmon sperm DNA,
and/or
the wash medium contains about 3 x SSC, 25 mM phosphate buffer pH 7.1, and 20% deionized formamide and wherein the probe used is anyone of the probes of claim 20, the hybridization temperature being suitable adjusted to the range of about 55°C and/or the wash temperature to the range of about 55°C, and particularly, wherein said target sequence and the corresponding relevant hybridization temperature (HT) and wash temperature (WT), respectively, are as follows:

AAGCCTGTCC AGAGGATGGG TGTGG

HT and/or WT: 55°C.

23. Kit for the detection in vitro of a large number, preferably all Bordetella pertussis strains in a biological sample, with said kit containing:

either

- at least one probe selected among any of those according to claim 20;
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a large number, preferably all strains of Bordetella pertussis to be carried out;
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least two probes, targeting the same nucleic acid molecule, and of which at least one is specific for Bordetella pertussis and which is selected from any one of the probes of claim 20,
- the buffer or components necessary for producing the buffer enabling hybridization reaction betw en these probes and the DNAs and/or RNAs of a strain of Bordetella pertussis to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least one probe selected among any of those according to claim 20, which is fixed to a solid support,
- the primers needed for performing enzymatical amplification of the DNA and/or RNA containing the target sequence of the above-mentioned probe, when appropriate,
- the buffer or components necessary for producing the buffers enabling enzymatical amplification

and/or enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Bordetella pertussis to be carried out,

- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate.

24. Probe for detecting one or more Haemophilus influenzae strains, containing:

- either a sequence belonging to a nucleic acid selected from the following group of nucleic acids and which includes from 15 to the maximum number of nucleotides of the selected nucleic acid:

Group HII1:

ACGCATCAAA TTGACCGCAC TT	HII1
AAGTGCGGTC AATTTGATGC GT	HII1IC
AAGUGCGGUC AAUUUGAUGC GU	HII1ICR
ACGCAUCAAA UUGACCGCAC UU	HII1R

Group HII2:

ACTTTGAAGT GAAAACTTAA AG	HII2
CTTTAAGTTT TCACTTCAAA GT	HII2IC
CUUUAAGUUU UCACUUCAAA GU	HII2ICR
ACUUUGAAGU GAAAACUUAA AG	HII2R

- or a variant sequence which distinguishes of any of the preceding sequences:
  - * either by addition to or removal from any of their respective extremities of one or several nucleotides;
  - * or changing within any of said sequences of one or more nucleotides;
  - * or both;

yet provided that in any of the above circumstances said probe still hybridizes with the same RNA or DNA target as the corresponding unmodified sequence.

25. Process for detecting Haemophilus influenzae strains in a biological sample, wherein said process

comprises contacting said biological sample - in which the nucleic acids (DNAs and/or RNAs) of the strains have been made accessible to hybridization, if need be, under suitable denaturation conditions, with said nucleic acid to be detected being possibly amplified using the polymerase chain reaction, with two primers, more preferably two more evolutionarily conserved primers, flanking the target sequence of the probe - with a probe according to anyone of claim 24 under conditions enabling hybridization between the probe and complementary nucleic acids of the Haemophilus influenzae strains, which may be present in the sample, and detecting the hybrids possibly formed, particularly with a probe hybridizing to both DNA and RNA of a Haemophilus influenzae strain which may be present in the biological sample.

26. Process for detecting Haemophilus influenzae, in a biological sample, according to claim 25, wherein: the hybridization medium contains about 3 x SSC, (SSC = 0.15 M NaCl, 0.015 M sodium citrate, pH 7.0) about 25 mM of phosphate buffer pH 7.1, 20% deionized formamide, 0.02% Ficoll, 0.02% bovine serum albumin, 0.02% polyvinylpyrrolidone, and about 0.1 mg/ml sheared, denatured salmon sperm DNA,
and/or
the wash medium contains about 3 x SSC, 25 mM phosphate buffer pH 7.1, and 20% deionized formamide and wherein the probe used is anyone of the probes of claim 24, the hybridization temperature being suitable adjusted to the range of about 35°C to 55°C and/or the wash temperature to the range of about 35°C to 55°C, and particularly wherein said target sequence and the corresponding relevant hybridization temperature (HT) and wash temperature (WT), respectively, are as follows:
AAGTGCGGTC AATTTGATGC GT

HT and/or WT: 55°C
CTTTAAGTTT TCACTTCAAA GT
HT and/or WT: 35°C

27. Kit for the detection in vitro of a large number, preferably all Haemophilus influenzae strains in a biological sample, with said kit containing:

either

- at least one probe selected among any of those according to claim 24,
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a large number, preferably all strains of Haemophilus influenzae to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least two probes, targeting the same nucleic acid molecule, and of which at least one is specific for Haemophilus influenzae and which is selected from any one of the probes of claim 24,
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Haemophilus influenzae to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least one probe selected among any of those according to claim 24, which is fixed to a solid support,
- the primers needed for performing enzymatical amplification of the DNA and/or RNA containing the target sequence of the above-mentioned probe, when appropriate,

- the buffer or components necessary for producing the buffers enabling enzymatical amplification and/or enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Haemophilus influenzae to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate.

28. Probe for detecting one or more Streptococcus pneumoniae strains, containing:

- either a sequence belonging to a nucleic acid selected from the following groups of nucleic acids and which includes from 15 to the maximum number of nucleotides of the selected nucleic acid:

Group SPI1:	
GTGAGAGATC ACCAAGTAAT GCA	SPI1
TGCATTACTT GGTGATCTCT CAC	SPI1IC
UGCAUUACUU GGUGAUCUCU CAC	SPI1ICR
GUGAGAGAUC ACCAAGUAAU GCA	SPI1R
Group SPI2	
AGGAACTGCG CATTGGTCTT	SPI2
AAGACCAATG CGCAGTTCCT	SPI2IC
AAGACCAAUG CGCAGUUCCU	SPI2ICR
AGGAACUGCG CAUUGGUCUU	SPI2R
Group SPI3	
GAGTTTATGA CTGAAAGGTC AGAA	SPI3
TTCTGACCTT TCAGTCATAA ACTC	SPI3IC
UUCUGACCUU UCAGUCAUAA ACUC	SPI3ICR
GAGUUUAUGA CUGAAAGGUC AGAA	SPI3R

- or a variant sequence which distinguishes of any of the preceding sequences:

* either by addition to or removal from any of their respective extremities of one or several nucleotides;
* or changing within any of said sequences of one or more nucleotides;
* or both;

yet provided that in any of the above circumstances said probe still hybridizes with the same RNA or DNA target as the corresponding unmodified sequence.

29. Process for detecting Streptococcus pneumoniae strains in a biological sample, wherein said process comprises contacting said biological sample - in which the nucleic acids (DNAs and/or RNAs) of the strains have been made accessible to hybridization, if need be, under suitable denaturation conditions, with said nucleic acid to be detected being possibly amplified using the polymerase chain reaction, with two primers, more preferably two more evolutionarily conserved primers, flanking the target sequence of the probe - with a probe according to anyone of claim 28 under conditions enabling hybridization between the probe and complementary nucleic acids of the Streptococcus pneumoniae strains, which may be present in the sample, and detecting the hybrids possibly formed, particularly with a probe hybridizing to both DNA and RNA of a Streptococcus pneumoniae strain which may be present in the biological sample.

30. Process for detecting Streptococcus pneumoniae, in a biological sample, according to claim 29, wherein: the hybridization medium contains about 3 x SSC, (SSC = 0.15 M NaCl, 0.015 M sodium citrate, pH 7.0) about 25 mM of phosphate buffer pH 7.1, 20% deionized formamide, 0.02% Ficoll, 0.02% bovine serum albumin, 0.02% polyvinylpyrrolidone, and about 0.1 mg/ml sheared, denatured salmon sperm DNA,
and/or

the wash medium contains about 3 x SSC, 25 mM phosphate buffer pH 7.1, and 20% deionized formamide and wherein the probe used is anyone of the probes of claim 28, the hybridization temperature being suitable adjusted to the range of about 45°C and/or the wash temperature to the range of about 45°C, and particularly wherein said target sequence and the corresponding relevant hybridization temperature (HT) and wash temperature (WT), respectively, are as follows:

TGCATTACTT GGTGATCTCT CAC
HT and/or WT: 45°C
AAGACCAATG CGCAGTTCCT
HT and/or WT: 45°C
TTCTGACCTT TCAGTCATAA ACTC
HT and/or WT: 45°C

31. Kit for the detection in vitro of a large number, preferably all Streptococcus pneumoniae strains in a biological sample, with said kit containing:

either

- at least one probe selected among any of those according to claim 28;
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a large number, preferably all strains of Streptococcus pneumoniae to be carried out;
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least two probes, targeting the same nucleic acid molecule, and of which at least one is specific for Streptococcus pneumoniae and which is selected from any one of the probes of claim 28,
- the buffer or components necessary for producing the buffer enabling hybridization reaction between

these probes and the DNAs and/or RNAs of a strain of Streptococcus pn umoniae to be carried out,

- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least one probe selected among any of thos according to claim 28, which is fixed to a solid support,
- the primers needed for performing enzymatical amplification of the DNA and/or RNA containing the target sequence of the above-mentioned probe, when appropriate,
- the buffers or components necessary for producing the buffers enabling enzymatical amplification and/or enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Streptococcus pneumoniae to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate.

32. Probe for detecting one or more Streptococcus agalactiae strains, containing:

- either a sequence belonging to a nucleic acid selected from the following groups of nucleic acids and which includes from 15 to the maximum number of nucleotides of the selected nucleic acid:

Group SAI1:	
AATCGAAAGG TTCAAATTGT T	SAI1
AACAATTTGA ACCTTTCGAT T	SAI1IC
AACAAUUUGA ACCUUUCGAU U	SAI1ICR
AAUCGAAAGG UUCAAAUUGU U	SAI1R
Group SAI2:	
GGAAACCTGC CATTTGCGTC TT	SAI2
AAGACGCAAA TGGCAGGTTT CC	SAI2IC

AAGACGCAAA UGGCAGGUUU CC	SAI2ICR
GGAAACCUGC CAUUUGCGUC UU	SAI2R

Group SAI3:

TCCACGATCT AGAAATAGAT TGTAGAA	SAI3
TTCTACAATC TATTTCTAGA TCGTGGA	SAI3IC
UUCUACAAUC UAUUUCUAGA UCGUGGA	SAI3ICR
UCCACGAUCU AGAAAUAGAU UGUAGAA	SAI3R

Group SAI4:

TCTAGTTTTA AAGAAACTAG GTT	SAI4
AACCTAGTTT CTTTAAAACT AGA	SAI4IC
AACCUAGUUU CUUUAAAACU AGA	SAI4ICR
UCUAGUUUUA AAGAAACUAG GUU	SAI4R

- or a variant sequence which distinguishes of any of the preceding sequences:
  - * either by addition to or removal from any of their respective extremities of one or several nucleotides;
  - * or changing within any of said sequences of one or more nucleotides;
  - * or both;

yet provided that in any of the above circumstances said probe still hybridizes with the same RNA or DNA target as the corresponding unmodified sequence.

33. Process for detecting Streptococcus agalactiae strains in a biological sample, wherein said process comprises contacting said biological sample - in which the nucleic acids (DNAs and/or RNAs) of the strains have been made accessible to hybridization, if need be, under suitable denaturation conditions, with said nucleic acid to be detected being possibly amplified using the polymerase chain reaction, with two primers, more preferably two more evolutionarily conserved primers, flanking the target sequence of the probe - with a probe according to anyone f claim 32 under

conditions enabling hybridization between the probe and complementary nucleic acids of the Streptococcus agalactiae strains, which may be present in the sample, and detecting the hybrids possibly formed, particularly with a probe hybridizing to both DNA and RNA of a Streptococcus agalactiae strain which may be present in the biological sample.

34. Process for detecting Streptococcus agalactiae, in a biological sample, according to claim 33, wherein:

the hybridization medium contains about 3 x SSC, (SSC = 0.15 M NaCl, 0.015 M sodium citrate, pH 7.0) about 25 mM of phosphate buffer pH 7.1, 20% deionized formamide, 0.02% Ficoll, 0.02% bovine serum albumin, 0.02% polyvinylpyrrolidone, and about 0.1 mg/ml sheared, denatured salmon sperm DNA,

and/or

the wash medium contains about 3 x SSC, 25 mM phosphate buffer pH 7.1, and 20% deionized formamide and wherein the probe used is anyone of the probes of claim 32, the hybridization temperature being suitable adjusted to the range of about 35°C to 45°C and/or the wash temperature to the range of about 35°C to 45°C, and particularly wherein said target sequence and the corresponding relevant hybridization temperature (HT) and wash temperature (WT), respectively, are as follows:

AACAATTTGA ACCTTTCGAT T

HT and/or WT: 35°C

AAGACGCAAA TGGCAGGTTT CC

HT and/or WT: 45°C

TTCTACAATC TATTTCTAGA TCGTGGA

HT and/or WT: 45°C

AACCTAGTTT CTTTAAAACT AGA

HT and/or WT: 37°C

35. Kit for the detection in vitro of a large number, preferably all Streptococcus agalactiae strains in a biological sample, with said kit containing:

either

- at least one probe selected among any of those according to claim 32;
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a large number, preferably all strains of Streptococcus agalactiae to be carried out;
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least two probes, targeting the same nucleic acid molecule, and of which at least one is specific for Streptococcus agalactiae and which is selected from any one of the probes of claim 32,
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Streptococcus agalactiae to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least one probe selected among any of those according to claim 32, which is fixed to a solid support,
- the primers needed for performing enzymatical amplification of the DNA and/or RNA containing the target sequence of the above-mentioned probe, when appropriate,
- the buffers or components necessary for producing the buffers enabling enzymatical amplification and/or enabling hybridization reaction between

these probes and th DNAs and/or RNAs of a strain of Streptococcus agalactiae to be carried out,

- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate.

36. Probe for detecting one or more Campylobacter jejuni and Campylobacter coli strains, containing a sequence from 15 to the maximum number of nucleotides derived from the 16S-23S rRNA spacer sequence shown in Fig. 10 or its complement provided that the probe, at the appropriate conditions, hybridizes exclusively with DNA and/or RNA from Campylobacter jejuni and Campylobacter coli strains and not with DNA and/or RNA from other organisms.

37. Process for detecting Campylobacter jejuni and Campylobacter coli strains in a biological sample, wherein said process comprises contacting said biological sample - in which the nucleic acids (DNAs and/or RNAs) of the strains have been made accessible to hybridization, if need be, under suitable denaturation conditions, with said nucleic acid to be detected being possibly amplified using the polymerase chain reaction, with two primers, more preferably two more evolutionarily conserved primers, flanking the target sequence of the probe - with a probe according to anyone of claim 36 under conditions enabling hybridization between the probe and complementary nucleic acids of the Campylobacter jejuni and Campylobacter coli strains, which may be present in the sample, and detecting the hybrids possibly formed, particularly with a probe hybridizing to both DNA and RNA of a Campylobacter jejuni or Campylobacter coli strain which may be present in the biological sample.

38. Kit for the detection in vitro of a large number, preferably all Campylobacter jejuni and Campylobacter coli strains in a biol gical sample, with said kit containing:

either

- at least one probe selected among any of those according to claim 36;
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a large number, preferably all strains of Campylobacter jejuni or Campylobacter coli to be carried out;
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least two probes, targeting the same nucleic acid molecule, and of which at least one is specific for Campylobacter jejuni and Campylobacter coli and which is selected from any one of the probes of claim 36,
- the buffer or components necessary for producing the buffer enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain of Campylobacter jejuni or Campylobacter coli to be carried out,
- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate,

or

- at least one probe selected among any of thos according to claim 36, which is fixed to a solid support,
- the primers needed for performing enzymatical amplification of the DNA and/or RNA containing the target sequence of the above-mentioned probe, when appropriate,
- the buffers or components necessary for producing the buffers enabling enzymatical amplification and/or enabling hybridization reaction between these probes and the DNAs and/or RNAs of a strain

of Campylobacter jejuni or Campylobacter coli to be carri d out,

- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate.

39. Process for the in vitro detection of one microorganism or to the simultaneous in vitro detection of several microorganisms contained in a biological sample using anyone of the probes according to claims 1 to 4, 8, 12, 16, 20, 24, 28, 32 and 36, and specific for the microorganism(s) to be detected wherein the DNA and/or RNA present in the biological sample (and comprising the target sequence) is labeled, preferably using enzymatic amplification with at least one set of primers flanking the probe region, and wherein said biological sample is contacted with a membrane on which one or more oligonucleotide probes are dot spotted on a known location, in a medium enabling specific hybridization of the amplified target sequence and the probes on the membrane and wherein the hybrids resulting from the hybridizations are detected by appropriate means.

40. Kit for the in vitro detection of one microorganism or for the simultaneous in vitro detection of several microorganisms contained in a biological sample, with said kit containing:

- at least one of the probes according to claims 1 to 4, 8, 12, 16, 20, 24, 28, 32 and 36, and specific for the microorganism(s) to be detected, which is dot spotted to a membrane,
- the primers needed for performing enzymatical amplification of the DNA and/or RNA containing the target sequence of the above-mentioned probe, when appropriate,
- the buffers or components necessary for producing the buffers enabling enzymatic amplification and/or enabling hybridization reaction between

these probes and the DNAs and/or RNAs of a microorganism or microorganisms which are to be detected to to be carried out,

- the means for detecting the hybrids resulting from the preceding hybridization, when appropriate.